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Abstract
While massively parallel sequencing of whole genomes shed light on many previously puzzling genetic questions, the high costs associated with this approach makes its use impractical when large cohorts need to be sequenced at high coverage. Available capture technologies reduces the sequencing costs by enriching template material for the regions of interest. However, these technologies are also prohibitively costly at high sample numbers. Capture methods utilizing molecular inversion probes (MIPs) offer a flexible alternative to enrich template material that multiplex well for thousands of samples and require minimal resources.

Here, for our work in malaria, we extend the utility of MIPs, improving the capture length and efficiency. We have also dramatically decreased the capture time from 24-48 h to 1 h. Combined, these improvements allow the potential for rapid and reliable application of MIP captures in research and, importantly, clinical settings.